INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification [6] : C12N 15/00, 15/12, C07K 14/00, 14/435	A1	(11) International Publication Number: WO 99/58660
		(43) International Publication Date: 18 November 1999 (18.11.99)

(21) International Application Number: PCT/US99/09847

(22) International Filing Date: 6 May 1999 (06.05.99)

(30) Priority Data:

60/085,093	12 May 1998 (12.05.98)	US
60/085,094	12 May 1998 (12.05.98)	US
60/085,105	12 May 1998 (12.05.98)	US
60/085,180	12 May 1998 (12.05.98)	US
60/085,927	18 May 1998 (18.05.98)	US
60/085,906	18 May 1998 (18.05.98)	US
60/085,924	18 May 1998 (18.05.98)	US
60/085,922	18 May 1998 (18.05.98)	US
60/085,923	18 May 1998 (18.05.98)	US
60/085,921	18 May 1998 (18.05.98)	US
60/085,925	18 May 1998 (18.05.98)	US
60/085,928	18 May 1998 (18.05.98)	US
60/085,920	18 May 1998 (18.05.98)	US

(71) Applicant (for all designated States except US): HUMAN GENOME SCIENCES, INC. [US/US]; 9410 Key West Avenue, Rockville, MD 20850 (US).

(72) Inventors; and
(75) Inventors/Applicants (for US only): RUBEN, Steven, M. [US/US]; 18528 Heritage Hills Drive, Olney, MD 20832 (US). FLORENCE, Kimberly [US/US]; 12805 Atlantic Avenue, Rockville, MD 20851 (US). NI, Jian [CN/US]; 5502 Manorfield Road, Rockville, MD 20853 (US). ROSEN, Craig, A. [US/US]; 22400 Rolling Hill Road, Laytonsville, MD 20882 (US). CARTER, Kenneth, C. [US/US]; 11601 Brandy Hall Lane, North Potomac, MD 20878 (US). MOORE, Paul, A. [US/US]; 19005 Leatherbark Drive, Germantown, MD 20874 (US). OLSEN, Henrik, S. [DK/US]; 182 Kendrick Place #24, Gaithersburg, MD 20878 (US). SHI, Yang-gu [CN/US]; 437 West Side Drive, Gaithersburg, MD 20878 (US). YOUNG, Paul, E. [US/US]; 122 Beckwith Street, Gaithersburg, MD 20878 (US). WEI, Fing-Fei [CN/US]; 242 Gravatt Drive, Berkeley, CA 94705 (US). BREWER, Laurie, A. [US/US]; Apartment 115, 410 Van Dyke Street, St. Paul, MN 55119-4321 (US). SOPPET, Daniel, R. [US/US]; 15050 Stillfield Place, Centreville, VA 22020 (US). LAFLEUR, David, W. [US/US]; 3142 Quesada Street, N.W., Washington, DC 20015 (US). ENDRESS, Gregory, A. [US/US]; 9729 Clagett Farm Drive, Potomac, MD 20854 (US). EBNER, Reinhard [DE/US]; 9906 Shelburne Terrace #316, Gaithersburg, MD 20878 (US).

(74) Agents: BROOKES, A., Anders et al.; Human Genome Sciences, Inc., 9410 Key West Avenue, Rockville, MD 20850 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZA, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published
With international search report.
Before the expiration of the time limit for amending the claims and to be republished in the event of the receipt of amendments.

(54) Title: 97 HUMAN SECRETED PROTEINS

(57) Abstract

The present invention relates to novel human secreted proteins and isolated nucleic acids containing the coding regions of the genes encoding such proteins. Also provided are vectors, host cells, antibodies, and recombinant methods for producing human secreted proteins. The invention further relates to diagnostic and therapeutic methods useful for diagnosing and treating disorders related to these novel human secreted proteins.

```
cgttatgggt tgaagtaatc cggactagcg cagccgggtt taaacgcagg cttcctgatt    600
gcctgggagg cctgttcata cccgtaggcg accgacagca acgtggcttc gctcaaattt    660
ttcccataga agtgaacggc tgtcggcatc ccttcgtcgt ccatgcccga tggtatggag    720
ataccgggat aaccggccac cgccgagtag tagtaactgt atgagtgaaa gttggacatc    780
attgcatcaa gcttatgctc ggccagcggc ttatcgatgg tgcttttgaa aatcgggccg    840
atggcagccc ataactcatt gcgcgcctca tcactgatat ccatcccgtt gatcatggtg    900
agcatctgtt gatccggcac acccggaccg ctgttgcgct cgttgaattc aatcagctca    960
gccagcgact tcaccggcaa gcctgcccgt ccggccaggt aggcttcaag ctggtgttta    1020
acgtccgata acaacgcgtc gttatattgt tcatgggttt cgtacgggac gccctcaccc    1080
agttgaccca cgggtaccaa tgtcgcgccc ttgcctcgca gcaacgtaat ggcatcctcg    1140
aagtgctsct gtcggctttt ttcgccgggt cgttggcatc ttctacagat aactcaggca    1200
acggcgtata accgatgcgc ttgcccacca aggcgtcagg cttgattccc tgggtgtagc    1260
ggttggtatc cgtcatcgca tccagtgctt gcgccgcatn acgcacgtta cgggtgaagg    1320
tgcccaccgt gtcctggcgg gaactggtca tcacccttcg gtactcacta atccttcggt    1380
cggtttgaaa ccaataacac cgttgtaagc cgccggcgta atgattgaac cattggtttc    1440
gaccccccaat gccaagggca caatcccttg tgcaacggct accgcagagc ccgtactcga    1500
g                                                                      1501
```

```
<210> 30
<211> 1752
<212> DNA
<213> Homo sapiens

<220>
<221> SITE
<222> (1099)
<223> n equals a,t,g, or c

<400> 30
aaggtacgcc tgcaggtacc ggtccggaat tcccgggtcg acccacgcgt ccgtccagga    60
cagagagtgc acaaactacc cagcacagcc ccctccgccc cctctggagg ctgaagaggg    120
attccagccc ctgccaccca cagacacggg ctgactgggg tgtctgcccc ccttgggggg    180
gggcagcaca gggcctcagg cctgggtgcc acctggcacc tagaagatgc ctgtgccctg    240
gttcttgctg tccttggcac tgggccgaag cccagtggtc ctttctctgg agaggcttgt    300
ggggcctcag gacgctaccc actgctctcc gggcctctcc tgccgcctct gggacagtga    360
catactctgc ctgcctgggg acatcgtgcc tgctccgggc cccgtgctgg cgcctacgca    420
cctgcagaca gagctggtgc tgaggtgcca gaaggagacc gactgtgacc tctgtctgcg    480
tgtggmtgtc cacttggccg tgcatgggca ctgggaagag cctgaagatg aggaaaagtt    540
tggaggagca gctgacttag gggtggagga gcctaggaat gcctctctcc aggcccaagt    600
cgtgctctcc ttccaggcct accctactgc ccgctgcgtc ctgctggagg tgcaagtgcc    660
tgctgccctt gtgcagtttg gtcagtctgt gggtctgtgg gtatatgact gcttcgaggc    720
tgccctaggg agtgaggtac gaatctggtc ctatactcag cccaggtacg agaaggaayt    780
caaccacaca cagcagctgc ctgactgcag ggggctcgaa gtctggaaca gcatcccgag    840
ctgctgggcc ctgccctggc tcaacgtgtc agcagatggt gacaacgtgc atctggttct    900
gaatgtctct gaggagcagc acttcggcct ctccctgtac tggaatcagg tccagggccc    960
cccaaaaccc cggtggcaca aaaacctgac tggaccgcag atcattacct tgaaccacac    1020
agacctggtt ccctgcctct gtattcaggt gtggcctctg gaacctgact ccgttagacg    1080
aacatctgcc ccttcaggna ggacccccgc gcacaccaga acctctggca agccgcccga    1140
ctgcgactgc tgaccctgca gagctggctg ctggacgcac cgtgctcgct gcccgcagaa    1200
gcggcactgt gctggcgggc tccgggtggg gacccctgcc agccactggt cccaccgctt    1260
tcctgggaca aygtcactgt ggacaaggtt ccgagttcc cattgctgaa aggccaccct    1320
aacctctgtg ttcaggtgaa cagctcggag aagctgcagc tgcaggagtg cttgtgggct    1380
gactccctgg ggcctctcaa agacgatgtg ctactgttgg agacacgagg cccccaggac    1440
aacagatccc tctgtgcctt ggaacccagt ggctgtactt cactacccag caaagcctcc    1500
acgagggcag ctcgccttgg agagtactta ctacaagacc tgcagtcagg ccagtgtctg    1560
cagctatggg acgatgactt gggagcgcta tgggcctgcc ccatggacaa atacatccac    1620
aagcgctggg ccctcgtgtg gctggcctgc ctactctttg cctgcgcttt ccctcatcct    1680
ccttctcaaa aaggatcacg cgaaagggtg gctgaggctc ttgaaacagg acgtccgctc    1740
gggggcggcc gc                                                         1752
```

```
<210> 31
<211> 2152
```

```
351  LeuGlnAlaCysSerTrpAlaAspSerLeuGlyProPheLysAspAspMe  367
     ::||||||||::||::|||||::|||||||:::|||||
701  CTGCAGGAGGTGCTTTGTGGGCTGACTCCTGGGCGCTTCAAAGACGATGT  750

367  tLeuLeuValGluMetLysThrGlyLeuAsnAsnThrSerValCysAlaL  384
     :|||||:::||||||||::|||      |||::|||||||||:||::
751  GCTACTGTTGGAGACAGAGGCCCCCAGGACAACACAGATCCCTCTGTGCCT  800

384  euGluProSerGlyCysThrProLeuProSerMetAlaSerThrArgAla  400
     :||||||||||||||||||||||::||||||::||||||||:
801  TGGAACCAGTGGGCTGTGACTTCACTACCCAGCAAAGCCTTCCACGAGGCA  850

401  AlaArgLeuGlyGluGluLeuLeuGlnAspPheArgSerHisGlnCysMe  417
     ||||:::|||||||||::::|||||::||:||||:::||||||
851  GCTCCCCTTGGAGAGTACTTACTACAGACCTGCCAGTCAGGCCAGTGTCT  900

417  tGlnLeuTrpAsnAspAspAsnMetGlySerLeuTrpProAlaCysProMetA  434
     ::||||||||||||||||||||::|||||::|:::||
901  GCAGCTAATGG..GACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGG  947

434  sPLysTyrIleHisArgArgTrpProLeuAlaCysSerLeuLeu  450
     ::||||||::|||::||:|||||||||::||||||||||
948  ACAAATACATCCACAACGCGTGGCCGCTGGCCTGCTCTACTC  997

451  LeuLeuAlaAlaLeuePhePheLeuLeuLeuLysLysAspArgArgGly  467
     ::|||||||||||||||||||||:||||||||||||||||::|||
998  TTTGCCGCTGCTTTCCCTCATCCTTCTCAAAAAGGATCACGCGAA  1047

467  s................................AlaAlaA  470
     ::||||||
1048 AGGGTGGCTGAGGCTCTTGAAACAGGACGTCCGCTCGGGGGGGGCCA  1097

470  rgGlySerArgThrAlaLeuLeuHisSerAlaAspGlyAlaGlyTyr  486
     ||||::|||||||||||||::|||::||||||||::|||:::
1098 GGGGC...CGCGCGGCTTCGCTCCTCTCACTACGGCGATGACTCGGGTTTC  1144

487  GluArgGluValGlyAlaAlaLeuAlaSerAlaAlaLeuSerGlnMetProLeuAr  503
     |||:::|||||||::|||||::::||||||||:::|||||||||
1145 GAGCGCGTCTGGTGGGCGGCCCCTGGCGTCGCCACTGCCCTACTC  1194

503  gValAlaValAlaAspLeuTrpSerArgArgGluLeuSerArgAlaHisGlyAlaL  520
     ::|||||||||::||||||||||||:::|||||||:::|||||
1195 CGTGGCGGCTGAGACCTGTGGAGCCGTCGTGAACTGAGCGCCAGGGGCCCG  1244

520  euAlaAlaTrpPheHisHisGlnArgArgIleLeuGluGlnGlyGlyVal  536
     ::|||||||||||||||||:::||||||||||||||||
1245 TGGCTTGGTTTCACGCGCCAGACCCTGCAGGAGGGCGCGTG  1294

537  ValIleLeuLeuPheSerProAlaAlaValAlaGlnCysGlnGlnTrpLe  553
     ::|||||||||||||:||||||||||::|||
1295 GTGGTCTTGCTTGCTTCTCTCCCGTGCGTGGGCGGACGGAGTGGGCT  1344

553  uGlnLeuGlnThrValGluPro..........GlyProHisAspAlaLeuA  567
     :::||:|||::|||||||
1345 ACAGGAANGGGGTGTCCGGGCCACAGGACCGCCTTCC  1394

567  laAlaTrpPheSerCysValLeuProAspPheLeuGlnGlyArgAlaThr  583
     ::||::|||||||||||||::|||||||:||||||||||:||
1395 GCGGCCTTCGCTCCAGCTGCCGTCTCCCCGACTTCTTNCAGGGCCGCGGCCC  1444

584  GlyAlaArgTyrValGlyValTyrPheAspGlyLeuLeuHisProAspSerVa  600
     :||||::|||||||||||||||||||:::||
1445 GGCAGCTACGTGGGGGTCTACTGCGACGGCCTGCTCCACCCGGACGCCGT  1494

600  lProSerProPheArgValAlaProLeuPheSerLeuProThrProGlnLeuP  617
     ||||:::||||||||::||||||:||||||
1495 ACCCGGCCCTTTCCGACACGTGCCGGTCGCTTCCTCCCAACTGC  1544

617  roAlaPheLeuAspAlaLeuLeuGlnGlyCysSerThrSerAlaGlyArg  633
     ||||||||||||||||::|||||||||
1545 CAGACTTCCTGGGACGCCCTGCAGCCCTGCAGCTCCGTTCCGGCGG  1594
```

```
634  ProAlaAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAs  650
     ::||::|||::|||||||||||:|||||||||||||||||
1595 CTCCAAGAGAGAGGAGCGGGAGCAAGTGTCCCGGGGCCCTTCAGCCAGCCACCCTGGA  1644

650  pSerCys.......ThrSerSerGluAlaProGly  660
     :::::              |||||||||
1645 TAGCTACTTCCATCCCCCGGGGACTCCCGGCCCGCGGGA  1681
```

seq_name: /SIDS1/gcgdata/geneseqn-embl/NA2000.DAT:AAZ65269

us-09-899-471-2.rng

```
CC  are most highly expressed in, and include developing products for the
CC  diagnosis or treatment of cancer, tumours, developmental abnormalities
CC  and foetal deficiencies, blood disorders, diseases of the immune system,
CC  autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
CC  disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
CC  disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC  disorders, digestive/endocrine disorders, infections and AIDS. The
CC  polypeptides are also useful for identifying their binding partners.
CC. The sequences shown in AAY76224 to AAY76224 represent fragments of the
XX  secreted proteins.
SQ  Sequence 1752 BP; 324 A; 555 C; 522 G; 347 T; 4 other;
```

```
alignment_scores:
         Quality:  1671.00          Length:      496
         Ratio:    4.157            Gaps:          5
Percent Similarity: 81.048    Percent Identity: 65.726

alignment_block:
US-09-899-471-2

Align seq 1/1   to: AAZ65269      .
               AAZ65269   from: 1   to: 1752
```

```
   1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgAsnProVa  17
     ||||||||||||||||||||||||:|||::||||||||||||||||||||
   1 ATGCCTGTGTCCTGGTTCTTGCTGTCTTGGCTGCGGAACCCAGT      276

  17 lvalValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCys  34
 277 GGTCCTTCTCTGGAGAGGGCTTGTGGGGCCCTCAGGACGGCTACCCACTGCT  326

  34 erLeuGlyLeuSerCysHisLeuTrpAspSerGlyAspValLeuCysPro  50
 327 CTCCGGCGCCTCTCCTGCCATCTGTGGGACAGTGACATACTCTGCCTGCCT  376

  51 GlySerLeuGlnSerAlaProGlyProValLeuValProThrArgLeuGl  67
 377 GGGGACAATCGTGCCTCCCGGCCCCCGTGCTGGTCCCTACGCACCTGCA   426

  67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysAlaLeuArgv  84
 427 GGGGACATCGTGCCTCTCCGGCCCCCGTGCTGGTCCCTACGCACCTGCA  476

  84 aLAargValValHisLeuAlaValHisGlyHisTrpIleAlaGluProGlu 100
 477 TGGCGTGTGGGMTGTCCACTTGGCCGTGCATGGGCACTGGGAAGAGCCTGAA 526

 101 Glu.........       AlaGlyLysSerAspSerGluLeuGlnLeuSerAr 113
 527 GATGAGGAAAAGTTGGAGGAACAGCRGACTTAGGGGTGGAGGAGCCTAG   576

 113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
 577 GAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCCTA 626

 130 leAlaArgCysAlaLeuLeuGluValGlnValProAlaAspLeuValGln 146
 627 CTGCCCGCTGCGTCCTCTGGAAGTGCAAGTGCCCTGCCCTTGTGCAG    676

 147 ProGlyGlnSerValGlySerAlaValPheAspCysPheGluAlaSerLe 163
 677 TTTGGTCAGTCTGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTCAGT   726

 163 uGlyAlaGluValGlnIleIleTrpSerArgTyrThrLysProArgTyrG 180
 727 AGGGAGCTGAGGTAGCAAATCGGTCTCCATAACTCAGCCCAGGTACGACAGG 776

 180 luLeuAsnLeuThrGlnGlnLeuPro............       188
 777 AAYTCAACCACACAGCAGCTGCCTGACTGCCAGGGGGGCTCGAAGTCTGG 826

 189 .................       As 189
```

```
 827 AACAGGCCATCCCGAGCTGCTGGGGCCCTGCCCCGGCCTCAACGGTGTCAGCAGA   876
 877 TGGTGACAACGTGCATCTGGGTTCTGAAATGTCTCTGGAGGAGGCAGCACTTCG   926
 977 CACAAAAAACCTGACTGGACCCGGAGATCATTACCTTGAACCACAGACCT      1026
1027 GGTTCCCTGCCCTTGTAATTCAGGTGTGCCTGTTGGGAACCTGGACTCCGTTA   1076
1126 TGGCAAGCCACGCGCCCGACTGCTGCCAGAGCCTGGCTGCCTGGA          1175
1176 CGCACCGTGCGTCGCTCCCCGAGAAGCGGCACTGGTCCCTGGGGCTCCGG     1225
1276 ACTGTGGGACACAAGGTTCTCGAGTTCCCATTGCTGAAAGCCCACCCTAACCT   1325
1376 GGGCTGACTCCCTGGGGCCCTCTCCAAAGACGATGTGCTACTGTTGGAGACA   1425
1476 TACTTCACTCACCCAGCGAAAGCCTCACGAGGGCCAGCTCGCCTTGGAGAGT    1525
1573 GATGACTTGGGAGCGGCTGTATGGGCGCTGCCCATGGGACAAAATACATCCACAA 1622
1623 GCGCTGGGCCCTCCGTGTGGCTGGCCGCCTCCTACTCTTTCGCCTGGGCT...T  1669
1670 TCCCTCCATCCCCTTCTCAAAAAGGATCACGCGCAAA 1705
```

276 oAspSerGluArgValGluPheCysProPheArgGluAspProGlyAlaH 293
    |||||||||
    TGACTCCGTTAGGACAGAACAATCTNGGCCCCTTCAGGGAGGAACCCCGCCAC
457 lsArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyVal 473
    |:||:|||
    ACCAGAACCTCTGGCAAGCCCGACTGGCTGACCCTGCAGAGC 506
293 lsArgAsnLeuTrpHisIleAlaArgLeuArgValLeuSerProGlyVal 309
    |:||:|||
    ACCAGAACCTCTGGCAAGCCCGACTGGCTGACCCTGCAGAGC 506
310 TrpGlnLeuAspAlaProCysCysLeuProGlyLysValThrLeuCysTr 326
    |||:|||:||
    TGGCGCTGCTGGACGCACGTGGCTCGCTCCGGGCTGTGCTG 326
343 lnLysAsnAlaThrValAlaAsnGluProGlnGlnLeuValAlaGly 359
    :::|||:|||
    GGGAGAACGTCACTGTGGAC 359
360 HisProAsnLeuCysValGlnValSerThrTrpGluLysValGlnLeuGl 376
    ||:|||
    GTGAACAGCTCGGAGAAGGTGCAGCTGCA 705
376 nAlaCysSerTrpProAlaAspSerLeuGlyProPheLysAspSerMetLeuL 393
    |||
    GGAGTGCTTGTGGGCTGACTCCTTGGGGCCTTCTCAAAAGACGATNGTGCTAC 755
393 euValGlnMetLysThrGlyLeuAsnAsnThrSerValCysAlaLeuGlu 409
    :::|||:|||
    TGTTGGACACGAGGCCCCAGGACAACAGATCCTCTGTGCCTTGGAA 805
410 ProSerGlyCysThrProLeuProSerMetAlaSerThrThrArgAlaAr 426
    |||:|||
    CCCAGTGGGCTGTACTTCACTACCCAGCAAAGCCTTCCACGAGGGCAGCTCG 855
426 gLeuGlyGluLeuGlnAspPheArgSerHisGlnCysMetGlnL 443
    |||:||
    CCTTGGAGAGTNACTTACTACAAGAACCTCCAGTCAGGCGCCAGTGTGTCGCAGC 905
443 euTrpAsnAspAspAsnMetGlySerLeuTrpIleProAlaCysProMeteAspPly 459
    TATGG
    GACGATGACTTGGAGCGCTATNGGGCCTGCCCCATGGACAAA 952
460 TyrIleHisArgArgTrpValTrpLeuAlaCysSerLeuLeuLeuL 476
    ::::|||:|||
    TACATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCTCTCTTTGC 1002
476 aAlaAlaLeuPhePheLeuLeuLeuLysLysLysAspArgArgLys 491
    :::|||:|||
    CGCTGCGCTTTCCCTCATCCTCCTTTCTCAAAAAGGATCACGCGAAAGGGT 1052
492 ....AlaAlaArgGly 495
    ||||||||
    ....AlaAlaArgGly 495
496 SerArgThrAlaLeuLeuLeuHisSerAlaAspGlyAlaGlyTyrGluAr 512
    |||||||||
    ...CGCCGGGGCTCTGCTCCTCTACTCACCGGATGACTCGGGTTTCCAGCCG 1149
512 gLeuValGlyAlaLeuAlaSerAlaLeuSerGlnMetProLeuArgValA 529
    |:||||||
    CCTGGTGGGGCGCCCTGGCGTCCACCTGCCCCTGCGGTGG 1199
529 laValAspLeuTrpSerArgArgGluLeuSerAlaHisGlyAlaLeuAla 545
    |||||||||
    CCGTAGACCTGTGGAGCCGTCGTGAACTGAGCGCGCAGGGCGCCCTGGCT 1249
546 TrpPheHisHisGlnArgArgIleLeuGlnGluGlyValValIll 562
    ||||||||
    TGGTTTCACGCGCGCCAGCGCCGCCAGAACCCTGCAGGAGGGCGGCGTGGTGGT 1299

seq_name: /SIDSl/gcgdata/geneseqn/geneseqn-embl/NA2000.DAT:AAZ65269

562 eLeuLeuPheSerProAlaAlaValAlaAlaGlnCysGlnGlnTrpLeuGlnL 579
    ||||||||
    CTTGCTCTTCTTCTCCCGCCGTNGCTGCTGCTGCAGCGAGTGGCTACAGG 1349
579 euGlnThrValGluPro.........GlyProHisAspAlaLeuAlaAlaAla 592
    |||
    ATGGGGTGTCCGGGCCCCCGGGGGCGCGGGCCCGCACACGGCCTTCCGGCGCC 1399
593 TrpLeuSerCysValLeuProAspProPheLeuGlnGlyArgAlaThrGlyAr 609
    |||||||||
    TCGCTCAGCTGGCTGCTCCCCGAGACTTCTTGCAGGGGCGCACGGGCAG 1449
609 gTyrrValGlyValTyrPheAspGlyLeuLeuHisProAlaSerValPro 626
    |||||||||
    CTACGTGGGGGGGGCTGCGTTCGACAGGCTGGTCCACCCGGTACCCG 1499
626 erProPheArgValAlaProLeuPheSerLeuProThrGlnLeuProAla 642
    ||||||||
    CCCTTTTCCGCACCGTGCCCGTCTTCACACTGCCCTCCAACTGCCCAGAC 1549
643 PheLeuAspAlaLeuGlnGlyGlyCysSerThrSerAlaGlyArgProAl 659
    :::|||
    TTCCTGGGGGCCCTGCACAGCGCTGGGCCCCGGCGTTCCGGGCGCTCCA 1599
659 aAspArgValGluArgValThrGlnAlaLeuArgSerAlaLeuAspSerC 676
    |||||||||
    AGAGACGGACGAGCAAGTNCTCCCGGGCGCCTTCAGCCAGCGCCCTGGATAGCT 1649
676 ys.........ThrSerSerSerGluAlaProGly 684
    :::||
    ACTTCCATCCCCCGGGGGACTCCCGCGCCGGGA 1681

```
5.
1200 C
546·TrpPF
1250 TGGTTTC
```

```
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Ruben SM, Florence K, Ni J, Rosen CA, Carter KC, Moore PA;
PI   Olsen HS, Shi Y, Young PE, Wei F, Brewer LA, Soppet DR;
PI   Lafleur DW, Endress GA, Ebner R;
XX
DR   WPI; 2000-062296/05.
DR   P-PSDB; AAY76143.
XX
PT   New isolated human genes and the secreted polypeptides they encode,
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders -
XX
PS   Claim 1; Page 308; 475pp; English.
XX
CC   AAZ65250 to AAZ65350 represent 97 isolated human secreted protein genes.
CC   This sequence was found to be present on human chromosome 3.
CC   AAY76124 to AAY76223 represent the secreted proteins encoded by the 97
CC   human genes. The genes and their corresponding secreted polypeptides are
CC   useful for preventing, treating or ameliorating medical conditions,
CC   e.g. by protein or gene therapy. Also pathological conditions can be
CC   diagnosed by determining the amount of the new polypeptides in a sample
CC   or by determining the presence of mutations in the new genes. Specific
CC   uses are described for each of the 97 genes, based on which tissues they
CC   are most highly expressed in, and include developing products for the
CC   diagnosis or treatment of cancer, tumours, developmental abnormalities
CC   and foetal deficiencies, blood disorders, diseases of the immune system,
CC   autoimmune diseases, inflammation, allergies, Alzheimer's and cognitive
CC   disorders, schizophrenia, arthritis, asthma, psoriasis, sepsis, skin
CC   disorders, atherosclerosis, diabetes, cardiovascular disorders, kidney
CC   disorders, digestive/endocrine disorders, infections and AIDS. The
CC   polypeptides are also useful for identifying their binding partners.
CC   The sequences shown in AAY76224 to AAY76424 represent fragments of the
CC   secreted proteins.
XX
SQ   Sequence 1752 BP; 324 A; 555 C; 522 G; 347 T; 4 other;
XX
```

```
alignment_scores:
        Quality:  1801.00                    Length:   496
        Ratio:    4.248                       Gaps:     4
        Percent Similarity: 85.484   Percent Identity: 69.556

alignment_block:
US-09-899-471-5 x AAZ65269

Align seg 1/1   to: AAZ65269        from: 1 to: 1752
```

```
  1 MetProValSerTrpPheLeuLeuSerLeuAlaLeuGlyArgGlnAsnProVa 17
    |||||||:
227 ATGCCTGTGCCCCTGGTTCTTCGTCTCCTGTGGCCGAAGCCCAGT 276

 17 lValValSerLeuGluArgLeuMetGluProGlnAspThrAlaArgCysS 34
    ||||||:||||||||||||||:||||||||:::
277 GGTCCTTCTTCCTCGAGAGGCTTGTGGGCCCTCAGGACCCTACCCACTGCT 326

 34 erLeuGlyLeuSerCysHisLeuTrpAspGlyAspValLeuCysLeuPro 50
    ||||:||||:||||:||||:||||:::||||:::
327 CTCCGGGCCCTCTCCTCCCGGCCTTCTGGGACAGGTGAACATACTCTGGCCT 376

 51 GlySerLeuGlnSerAlaProGlyProValLeuProThrArgLeuGl 67
    |||||::||:|:|||:
377 GGGGACAATCCGTGCCCTCCTCCCGGCGCCCCGTGCTGGCCGCACCTGCA 426

 67 nThrGluLeuValLeuArgCysProGlnLysThrAspCysSerAlaLeuArgV 84
    |||||||||||||::|||||:||:||||:
427 GACACAGAGCTGGTGCTGCGAGGTCCCAGAAGACACCGACCTGACCCTGTC 476

 84 aIArgValValValHisLeuAlaValHisGlyHisTrpPAlaGlyProGlu 100
    :||||||||||||||:||||:||:|||:::||:
477 TGCGGTGTGGMGTCCACTTGGCCGTGCATGGGCCACTGGGAAGAGCCTGAA 526

101 Glu............AlaGlyLysSerAspSerGluLeuGlnGluSerAr 113
    :::|||
527 GATGAGGAAAAGTTTGGAGGACGAGCGTGGACTTAGGGGTGGAGAGCCTAG 576

113 gAsnAlaSerLeuGlnAlaGlnValValLeuSerPheGlnAlaTyrProI 130
    |||::|||||||||:||||||||||:::::||:
577 GAATGCCTCTCCTCCAGGCCCAAGTCGTTGCTCTCCTTCCAGGCCTACCCTA 626

130 leAlaAsnArgCysAlaLeuLeuGluValGlnuValProAlaAspLeuValGln 146
    |||:|||:||||||:||||||:::||||||||||:
627 CTGCCCGCCTCGGTCCTGCGAGGTGCAAAGTGCCTGCTCCCCTTGTGCAG 676

147 ProGlyGlnServalGlySerAlaValAlaPheAspCysPheGluAlaSerLe 163
    ::||||||::|||||:||||||:
677 TTTGGGTCAGTCGTGTGGGGCTTCTGTGGTATATGACTGCTTCGAGGCTGCCT 726

163 uGlyAlaGlyLeuValGlnIleLeuTrpSerThrTyrThrLysProArgTyrGlnLysG 180
    |||:|||:||:||:|||:::||:|||||||||||||||:::::|||:
727 AGGGAGTGGAGGTAGCAGAAATCTGGTCCTATACTACTCAGCCCCAGGTACGGAAGG 776

180 luLeuAsnLeuThrGlnGlnLeuProAspCysArgGlyLeuGluGlyValArg 196
    ||:|:||:|||||||||||||||:||||||:||:||||||||||:
777 AAYTCAACCACACACAGCCAGCTGCCTGACTGCAGGGGGCTCGAAGTCTGG 826

197 AspSerIleGlnSerCysTrpValLeuProTrpLeuAsnValSerThrAs 213
    :::||||:|||||||||||||:::|||:|||:||||||:
827 AACACGGATCCCGAGCTGCTGGGCCCTTGGCTCAACGTGTCAGCAGA 876

213 pGlyAspAsnValLeuLeuThrLeuAspValSerGluGluGluLeuAspPhes 230
    ::::|||||||||||||:||||||||::|||||||::|||
877 TGGTGACAACGTGCAICTGGTTCTGAANCTCTCTGGAGGAGGACAGCACTTCG 926

230 erPheLeuLeuTyrLeuArgProValProAspProAlaLeuLeuLysSerLeuTrp 246
    |||||||||||:||||||||||||:::|||
927 GCCTTCCCCTGTACTGAATCAGGTTCAGGGCCCCCAAAAACCCGGTGG 976

247 TyrLysAsnLeuThrGlyProGlnAsnIleThrLeuAsnHisThrAspLe 263
    ::::|||:::|||||||||||||||||||||||||||||||||||
977 CACAAAAACCTGACTGGACCCGCAGATCATTACCTTGAACCACACAGACCT 1026

263 uValProCysLeuCysIleGlnValTrpSerThrLeuGluProGlyAspSerGluA 280
    ||||:::|||||:::|||::||:
1027 GGTTCCCTGCCTCTGTAATCAGGTGTGGCCCTTGGAACCTGAGAGCTCCGTTA 1076

280 rgValGluPheCysProPheArgGluAspProGlyAlaIleHisArgAsnLeu 296
    :|:|||||||||||||||||:::||:
1077 GACG.AACATCTGCCCCTTCAGGNAGAACCCCGCGCACACAGAACCTC 1125

297 TrpHisIleAlaArgLeuArgValLeuSerProGlyValTrpGlnLeuAs 313
    ||||:::|||||||||||||||::|||||
1126 TGGCCAAGCACCGCCGCCGACTGCGAGTTCCCAGCCCGGGTGCTGGA 1175

313 pAlaProCysCysSerLeuProGlyLysValThrLysCysTrpPGlnIleAlaProA 330
    ||||||||||:||||||||||||||:||||||||:::||:
1176 CGCACCGTGCTCGCCTGCCCCGCAGAAGCGCACTGTGCCTGCTGGGGTCCGG 1225

330 spGlnSerProCysGlnProLeuValProProValProGlnLysAsnAla 346
    :::||||||||||||:::||:::|||::|:::
1226 GTGGGGACCCTTGCCAGCCACTGGGTCCCACCGCTTTTCCTGGGAAAYGTC 1275

347 ThrValAsnGluProGlnAspPheGlnIleuValAlaAlaGlyHisProAsnLe 363
    ||||||||||||:::|||:||||||||||||||||:
1276 ACTGTGGACAAGGTTTCTCGAGTTCCCATTGCTCAGAAAAGGCCACCCTAAACCT 1325

363 uCysValGlnValSerThrHrTrpGluValGlnLeuGlnLeuAlaCysSerT 380
    ||:::||:|||||||:|||::|||||||||||||||||||||||
1326 CTGTGTTCAGGTGAACAAGCTCGGAGAACCTGCAGCTGCAGGAGYGCTTGT 1375

380 rpAlaAspSerProGlyLeuProPheLysAspAspSerMetLeuLeuValGluMet 396
    :|||||||||||:::||:::||:::|:||:::||||:::
1376 GGGCCTGGACTCCCCTGGGGGCCTTCAAAACGACGATGTGCTACTGTTGGGAGACA 1425

397 LysThrGlyLeuAsnAsnThrSerValCyssAlaLeuGluLeuGluProSerGlyCy 413
    :::|||||||||||||||||||||||||
```